Supplementary Material

Disentangling scalar coupling patterns by real-time SERF NMR

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Experimental

Cyclo-Phe-Pro was obtained from Bachem AG (Bubendorf, Switzerland). All other chemicals were purchased from by Sigma-Aldrich (St. Louis, MO, USA) at > 98% purity. All experiments were carried out on a Bruker AVANCE III 500 MHz spectrometer using a 5 mm TXI probe with z-axis gradients at 298 K.

One-dimension real-time SERF spectra were obtained using a 60 ms EBURP-2 pulse for sliceselective excitation during a weak pulsed field gradient of 1.5 G/cm. During the interrupted acquisition we used 10-15 ms 180° Gaussian pulses for refocusing and two 270° Gaussian pulses of 10 ms each, for selective recoupling. A total of 80 individual FID data chunks of 25 ms were added up automatically during acquisition, resulting in a total acquisition time of ~ 2 s.

Computational details

Starting from the X-ray structure of cyclo-Phe-Pro (CITXAE12 [1,2]) a conformational search using the mixed torsion/low-frequency-mode Monte Carlo sampling with CHCl₃ as the solvent, as implemented in Maestro [3] in combination with the OPLS 2005 force field [4] was performed. The resulting 5 unique conformations within an 5 kcal mol⁻¹ window were then re-optimized with the dispersion-corrected B97D density functional [5] and the 6-31G(d,p) basis set using Gaussian 09 [6]. Solvent effects (DMSO) were approximated using the SMD solvation model [6]. All structures were characterized by frequency calculations and thermochemical data were obtained by the standard rigid-rotor harmonic-oscillator approximation. Final relative Gibbs free energies used for Boltzmann-weighting are based on LPNO-CEPA/1 calculations [7-10] using the def2-TZVPP [11,12] basis set combined with B97D/6-31G(d,p) thermal corrections based on Grimme's quasi-RRHO approach [13] to estimate entropic contributions from low-frequency vibrations (v < 100 cm⁻¹; $\alpha = 4$ and $B_{av} = 10^{-44}$ kgm⁻¹). Finally, SMD-B97D/6-31G(d,p) solvation (DMSO) energies were added. NMR coupling constants were calculated using the pcJ-2 basis set [14] and weighted by the Boltzmann factor of the individual conformations. Programs used were Gaussian 09 [15] and ORCA [16,17].



Figure S1: A regular 1D ¹H spectrum (bottom) and two single scan real-time SERF spectra of a solution of 8 mg n-propanol in 600 μ l DMSO-d₆, recorded at 310 K on a Bruker Avance III 500 MHz NMR spectrometer without cryo probe. The selectively refocused signals are indicated by the wavy arrows.

Supporting References

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```
;avance-version
;1D sequence with explicit programming of acquisition
;$CLASS=HighRes
;$DIM=1D
;$TYPE=
;$SUBTYPE=
;$COMMENT=
#include <Avance.incl>
#include <De.incl>
#include <Grad.incl>
#include <Delay.incl>
dwellmode explicit
"d11=3u"
"d12=6.5u"
"d20=10u"
"d2=aq/10"
"d3=d2/2"
"11=10-1"
"p2=2*p1"
1 ze
2 3m
 4u BLKGRAD
  d1 rpp2
 50u UNBLKGRAD
  d12 pl0:f1
  d12 gron1
  (p12:sp12 ph1)
  d12 groff
  d12 pl1:f1
  ACQ START (ph30, ph31)
   0.05u DWL_CLK_ON
   0.1u REC UNBLK
   d3:r
   0.1u REC BLK
   0.05u DWL_CLK_OFF
   p16:gp2
   d16 pl0:f1
   10u
   (p24:sp24 ph14)
```

10u d16 pl1:f1 p2 ph2 d16 pl0:f1 10u (p24:sp24 ph14) 10u p16:gp3 d16 1m d16 pl0:f1 10u dll gronl (p13:sp13 ph3) dll groff 10u p16:gp4 d16 3 0.05u DWL CLK ON 0.1u REC_UNBLK d2:r 0.1u REC BLK 0.05u DWL_CLK_OFF p16:gp2 d16 pl0:f1 10u (p24:sp24 ph14) 10u d16 pl1:f1 p2 ph2 d16 pl0:f1 10u (p24:sp24 ph14) 10u p16:gp3 d16 1m d16 pl0:f1 10u dll gronl (p13:sp13 ph3) dll groff 10u p16:gp4 d16 lo to 3 times 11

```
0.05u DWL CLK ON
   0.1u REC UNBLK
   d3:r
   25m
   0.1u REC BLK
   0.05u DWL CLK OFF
rcyc=2
wr #0
exit
;ph1 = 0
;ph2 = 0
; ph31 = 0
; ph30 = 0
ph1 =0 2 2 0 1 3 3 1
ph2 = 0 2
ph3 = 2 0
ph14 = 0 \ 0 \ 2 \ 2
ph30=0
ph31=0 2 2 0 1 3 3 1
;pl1 : f1 channel - power level for pulse (default)
;p1 : f1 channel - high power pulse
;d1 : relaxation delay; 1-5 * T1
;d7 : Serf delay
;NS: 1 * n, total number of scans: NS * TD0
;120:
;$Id: zgadc,v 1.12 2009/07/02 16:40:47 ber Exp $
```

8